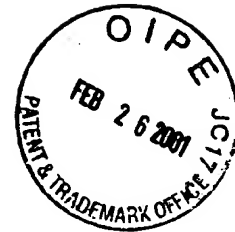


SEQUENCE LISTING



<110> ABRIGNANI, SERGIO  
GRANDI, GUIDO

<120> HEPATITIS C RECEPTOR PROTEIN

<130> PP00366.103

<140> US 09/509,612

<141> 2000-03-29

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5

<210> 3

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38

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Leu Lys Gly Ser Phe Leu Asp Asp  
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47

<210> 8  
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<220>  
<223> Description of Artificial Sequence:peptide

<400> 8  
His His His His His Leu Lys Gly Ser Phe  
1 5 10

<210> 9  
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Sequence:oligodeoxynucleotides

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cggttccgca gaccactatg

<210> 10  
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Sequence:oligodeoxynucleotides

<400> 10 21  
tcttcacgca gaaagcgtct a

<210> 11  
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Sequence:oligodeoxynucleotide

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tgagtgtcgt gcagcctcca gga

<210> 12  
<211> 357  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Human EC2  
fragment cloned into pThio-His C

<400> 12

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ggcatgctga gctcgagctt tgtcaacaag gaccagatcg ccaaggatgt gaagcagttc 120  
tatgaccagg ccctacagca ggccgtggtg gatgatgacg ccaacaacgc caaggctgtg 180  
gtgaagacct tccacgagac gcttgactgc tgtggctcca gcacactgac tgctttgacc 240  
acctcagtgc tcaagaacaa tttgtgtccc tcgggcagca acatcatcag caacctcttc 300  
aaggaggact gccaccagaa gatcgatgac ctcttctccg ggaagctgtg aaagctt 357

<210> 13

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Deduced amino acid sequence of EC2 fragment

<400> 13

Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly Ser Gly Asp Asp Asp  
1 5 10 15

Asp Lys Val Pro Gly Met Leu Ser Ser Ser Phe Val Asn Lys Asp Gln  
20 25 30

Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala  
35 40 45

Val Val Asp Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe  
50 55 60

His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr  
65 70 75 80

Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile  
85 90 95

Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe  
100 105 110

Ser Gly Lys Leu  
115

<210> 14

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide sequence of EC20His6 fragment cloned into pGEX-KG

<400> 14

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aaggaccaga tcgccaagga tgtgaagcag ttctatgacc aggccctaca gcaggccgtg 120

gtggatgatg acgccaacaa cgccaaggct gtggtgaaga ccttccacga gacgcttgac 180  
 tgctgtggct ccagcacact gactgctttg accacctcag tgctcaagaa caatttgtgt 240  
 ccctcgggca gcaacatcat cagcaacctc ttcaaggagg actgccacca gaagatcgat 300  
 gacctcttct ccggaagct gcatcatcat catcatcatt gaaagctt 348

<210> 15  
 <211> 113  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Deduced amino  
 acid sequence of EC2-His 6 fragment

<400> 15  
 Leu Val Pro Arg Gly Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile  
 1 5 10 15  
 Leu Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr  
 20 25 30  
 Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala  
 35 40 45  
 Lys Ala Val Val Lys Thr Phe His Glu Thr Leu Asp Cys Cys Gly Ser  
 50 55 60  
 Ser Thr Leu Thr Ala Leu Thr Thr Ser Val Leu Lys Asn Asn Leu Cys  
 65 70 75 80  
 Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe Lys Glu Asp Cys His  
 85 90 95  
 Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu His His His His His  
 100 105 110  
 His

<210> 16  
 <211> 236  
 <212> PRT  
 <213> Pan troglodytes

<400> 16  
 Met Gly Val Glu Gly Cys Thr Lys Cys Ile Lys Tyr Leu Leu Phe Val  
 1 5 10 15  
 Phe Asn Phe Val Phe Trp Leu Ala Gly Gly Val Ile Leu Gly Val Ala  
 20 25 30  
 Leu Trp Leu Arg His Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu  
 35 40 45

Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile  
 50 55 60  
 Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys  
 65 70 75 80  
 Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr  
 85 90 95  
 Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly  
 100 105 110  
 Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp  
 115 120 125  
 Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala Lys  
 130 135 140  
 Ala Val Val Lys Thr Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser  
 145 150 155 160  
 Thr Leu Thr Ala Leu Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro  
 165 170 175  
 Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln  
 180 185 190  
 Lys Ile Asp Asp Phe Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala  
 195 200 205  
 Ala Ile Val Val Ala Val Ile Met Ile Phe Glu Met Ile Leu Ser Met  
 210 215 220  
 Val Leu Cys Cys Gly Ile Arg Asn Ser Ser Val Tyr  
 225 230 235  
 <210> 17  
 <211> 236  
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 <400> 17  
 Met Gly Val Glu Gly Cys Thr Lys Cys Ile Lys Tyr Leu Leu Phe Val  
 1 5 10 15  
 Phe Asn Phe Val Phe Trp Leu Ala Gly Gly Val Ile Leu Gly Val Ala  
 20 25 30  
 Leu Trp Leu Arg His Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu  
 35 40 45  
 Leu Gly Asp Lys Pro Ala Pro Asn Thr Ser Tyr Val Gly Ile Tyr Ile  
 50 55 60

Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys  
 65 70 75 80  
 Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr  
 85 90 95  
 Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly  
 100 105 110  
 Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp  
 115 120 125  
 Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala Lys  
 130 135 140  
 Ala Val Val Lys Thr Phe His Glu Thr Val Asp Cys Cys Gly Ser Ser  
 145 150 155 160  
 Thr Leu Ala Ala Leu Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro  
 165 170 175  
 Ser Gly Ser Asn Ile Ile Ser Asn Leu Leu Lys Lys Asp Cys His Gln  
 180 185 190  
 Lys Ile Asp Asp Phe Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala  
 195 200 205  
 Ala Ile Val Val Ala Val Ile Met Ile Phe Glu Met Ile Leu Ser Met  
 210 215 220  
 Val Leu Cys Cys Gly Ile Arg Asn Ser Ser Val Tyr  
 225 230 235  
 <210> 18  
 <211> 236  
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 Phe Asn Phe Val Phe Trp Leu Ala Gly Gly Val Ile Leu Gly Val Ala  
 20 25 30  
 Leu Trp Leu Arg His Asp Pro Gln Thr Thr Ser Leu Leu Tyr Leu Glu  
 35 40 45  
 Leu Gly Asp Arg Pro Ala Pro Ser Thr Phe Tyr Val Gly Ile Tyr Ile  
 50 55 60  
 Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys  
 65 70 75 80

Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr  
 85 90 95  
 Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly  
 100 105 110  
 Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp  
 115 120 125  
 Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala Lys  
 130 135 140  
 Ala Val Val Lys Thr Phe His Glu Thr Leu Asn Cys Cys Gly Ser Asn  
 145 150 155 160  
 Ala Leu Thr Ala Leu Thr Thr Ser Val Leu Lys Asn Ser Leu Cys Pro  
 165 170 175  
 Ser Gly Thr Asn Ile Phe Asn Ser Leu Met Lys Glu Asp Cys His Gln  
 180 185 190  
 Lys Ile Asp Glu Leu Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala  
 195 200 205  
 Ala Ile Val Val Ala Val Ile Met Ile Phe Glu Met Ile Leu Ser Met  
 210 215 220  
 Val Leu Cys Cys Gly Ile Arg Asn Ser Ser Val Tyr  
 225 230 235  
 <210> 19  
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 <212> PRT  
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 Phe Asn Phe Val Phe Trp Leu Ala Gly Gly Val Ile Leu Gly Val Ala  
 20 25 30  
 Leu Trp Leu Arg His Asp Pro Gln Thr Thr Thr Leu Leu Tyr Leu Glu  
 35 40 45  
 Leu Gly Asp Lys Pro Ala Pro Ser Thr Phe Tyr Val Gly Ile Tyr Ile  
 50 55 60  
 Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys  
 65 70 75 80  
 Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr  
 85 90 95



Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly  
 100 105 110

Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp  
 115 120 125

Gln Ala Leu Gln Gln Ala Val Met Asp Asp Asp Ala Asn Asn Ala Lys  
 130 135 140

Ala Val Val Lys Thr Phe His Glu Thr Leu Asn Cys Cys Gly Ser Asn  
 145 150 155 160

Thr Leu Thr Thr Leu Thr Thr Ala Val Leu Arg Asn Ser Leu Cys Pro  
 165 170 175

Ser Ser Ser Asn Ser Phe Thr Gln Leu Leu Lys Glu Asp Cys His Gln  
 180 185 190

Lys Ile Asp Glu Leu Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala  
 195 200 205

Ala Ile Val Val Ala Val Ile Met Ile Phe Glu Met Ile Leu Ser Met  
 210 215 220

Val Leu Cys Cys Gly Ile Arg Asn Ser Ser Val Tyr  
 225 230 235

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 <211> 236  
 <212> PRT  
 <213> Mus musculus

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 20 25 30

Leu Trp Leu Arg His Asp Pro Gln Thr Thr Ser Leu Leu Tyr Leu Glu  
 35 40 45

Leu Gly Asn Lys Pro Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile  
 50 55 60

Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys  
 65 70 75 80

Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr  
 85 90 95

Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly  
 100 105 110

Phe	Val	Asn	Lys	Asp	Gln	Ile	Ala	Lys	Asp	Val	Lys	Gln	Phe	Tyr	Asp	115	120	125
Gln	Ala	Leu	Gln	Gln	Ala	Val	Met	Asp	Asp	Asp	Ala	Asn	Asn	Ala	Lys	130	135	140
Ala	Val	Val	Lys	Thr	Phe	His	Glu	Thr	Leu	Asn	Cys	Cys	Gly	Ser	Asn	145	150	155
Ala	Leu	Thr	Thr	Leu	Thr	Thr	Thr	Ile	Leu	Arg	Asn	Thr	Leu	Cys	Pro	165	170	175
Ser	Gly	Gly	Asn	Ile	Leu	Thr	Pro	Leu	Leu	Gln	Gln	Asp	Cys	His	Gln	180	185	190
Lys	Ile	Asp	Glu	Leu	Phe	Ser	Gly	Lys	Leu	Tyr	Leu	Ile	Gly	Ile	Ala	195	200	205
Ala	Ile	Val	Val	Ala	Val	Ile	Met	Ile	Phe	Glu	Met	Ile	Leu	Ser	Met	210	215	220
Val	Leu	Cys	Cys	Gly	Ile	Arg	Asn	Ser	Ser	Val	Tyr					225	230	235